# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/559,0/3A
ATTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWA
IWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequen <210> sequence id number <400> sequence id number 000
(NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent:
Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence
	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules
"bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence

AMC - Biotechnology Systems Branch - 06/04/2001

RAW SEQUENCE LISTING

19 <170> SOFTWARE: FastSEQ for Windows Version 3.0

DATE: 07/27/2001 TIME: 11:32:09

PATENT APPLICATION: US/09/559,013A

Input Set : A:\473195\_1.txt

Output Set: N:\CRF3\07272001\I559013A.raw

Does Not Comply 3 <110> APPLICANT: Ono, Toshiro Corrected Diskette Needed Nakayama, Eiichi 6 <120> TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES THEREFOR 9 <130> FILE REFERENCE: L0461/7086 pr 1-3 11 <140> CURRENT APPLICATION NUMBER: US 09/559,013A 12 <141> CURRENT FILING DATE: 2000-04-26 14 <150> PRIOR APPLICATION NUMBER: US 60/168,353 15 <151> PRIOR FILING DATE: 1999-12-01 17 <160> NUMBER OF SEQ ID NOS: 32

### ERRORED SEQUENCES

	143	<210> SEQ ID NO: 5					
	144	<211> LENGTH: 1705					
	145	<212> TYPE: DNA					
	146	<213> ORGANISM: Mus mu					
	148	<400> SEQUENCE: 5					
	149	gccgcggtga gggaagtgg	a cgcgatggcc	gggtccgcgt	gggtgtccaa	ggtctctcgg	60
	150	ctgctgggtg cattccacaa	a cacaaaacag	gtgacaagag	gttttgctgg	tggtgttcag	120
	151	acagtaactt taatteetg	g agatggaatt	ggcccagaaa	tttcagcctc	agtcatgaag	180
	152	atttttgatg ctgccaaag					240
	153	ggaccaggag gaaagtggat	gateceteca	gaagccaagg	agtccatgga	taagaacaag	300
	154	atgggcttga aaggcccact					360 <sub>.</sub>
	155	ttgcttcgta agacatttga					420
	156	tataaaaccc cttacacgga					480
	157	tacagtggaa ttgagcatg					540
	158	gaagaagcaa gcaagcgcat					600
E>	159	accacgtcac (ngctgtgcac	c aaaagctaac	atcatgagga	tgtcagatgg	gctctttctg	660 / 1200
	160	caaaaatgca gggaaattt	g cggaagaact	gtaaagactt	aaatttaacg	agatgtactt	320 tem 9
E>	161	ggatactgtn gtttaaata	gggtanaag	accontccaa	tttgatgttc	ttgtcatgcc	780
	162	aaatttatac ggagacatco	ttagtgatct	gtgtgcagga	ctgattggag	gtcttggggt	840 m Ever
	163	gactccaagt ggcaatatt	g gagccaacgg	tgttgccatc	tttgaatcgg	ttcatggaac	900
	164	agccccggac attgcaggca	aggacatggc	caaccccacg	gccctcctgc	ttagtgctgt	960 Jumay
	165	gatgatgctt cgccacatg	g gactttttga	ccatgcagca	aaaatcgagg	ctgcatgttt	1020
	166	tgctacaatt aaggatggaa	a agagcttaac	aaaagatctg	ggaggcaacg	cgaagtgctc	1080 free
	167	tgacttcaca gaagaaatc	gtcgtagagt	caaagactta	gattagcact	cctgctggtg	1140
	168	gatttgctgc agtcagtcaa	tcactccaaa	aggataccct	gtaatcctcc	ttgagggcgc	1200
	169	ccaccattgg- <del>tttgcttgg</del>					1260
E>		caaaaccctt tgcaatggat					1320 den 9
E>			ttgtcccgtc	tgggtaaacn	ttattttgta	aactgtaagt	1380
	172	gaactgtatc atttatcatt	gttaacccat	tttacacttc	aggcaaaatc	attitectea	1440
	173	actgtaaata ttctgataca	ı gaattaataa	gagaagatat	ttaacttttt	aacaaaagcc	1500
	174	ctggattttt ggtttatgaa					1560
	175	agataacatt attctaata	c taatgggtac	aaaagaaatt	tactgggaaa	gttcacagca	1620

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	176 177 179		taata	aaa a	aatg	taag				a aa	taaaq	gtat	ttg	teet	ata (	catg	aattac		680 705	
	180	<2112	> LE	NGTH	: 23	3														
	181	<212> TYPE: PRT																		
	182	<213	> OR	GANI	SM: 1	Mus 1	nusci	ulus												
	184	<400	> SE	QUEN	CE:	6														
	185	Ala	Ala	Val	Arg	Glu	Val	Asp	Ala	Met	Ala	Gly	Ser	Ala	Trp	Val	Ser			
	186	1				5					10					15				
	187	Lys	Val	Ser	Arg	Leu	Leu	Gly	Ala	Phe	His	Asn	Thr	Lys	Gln	Val	$\mathtt{Thr}$			
	188		·		20					25				_	30					
	189	Arg	Gly		Ala	Gly	Gly	Val		Thr	Val	Thr	Leu		Pro	Gly	Asp			
	190			35				_	40	_	•		_	45		_		,		
	191	Gly		Gly	Pro	Glu	Ile		Ala	Ser	Val	Met		Ile	Phe	Asp	Ala			
	192	- 1	50		_	- 1	<b>a</b> 1	55	<b>a</b> 1	<b>a</b> 1	_	•	60	ml		<b>~1</b> -	<b>a</b> 1			
	193		ьуs	Ата	Pro	TTE		Trp	GIU	Glu	Arg		Val	Thr	Ата	ile			•	
	194	65	D	01	<b>01</b>	T	70	Wat	т1.	Dwa	Dwa	75	7.1.0	T 0	C1.,	000	80 Mot			
	195 196	GTĀ	Pro	СТУ	СТА	ьуs 85	ттр	met	TTE	Pro	90	GIU	Ala	ьуѕ	GIU	95	мес			
	197	λan	Tvc	λan	Lvc		C117	LOU	Twe	Gly		LOU	T 17.0	Thr	Dro		λla			
	198	АБР	пуз	ASII	100	Mec	σтў	Leu	цуз	105	FIO	Бец	пуз	1111	110	116	AIG			
	199	Δla	Glv	Hic		Ser	Mot	Δcn	T.011	Leu	Leu	Δrσ	T.vg	Thr		Δsn	T.011			
	200	Alu	GLY	115	110	UCI	rice	MOII	120	пси	ЦСИ	1119	шуы	125	1 110	115P	Dea			
	201	Tvr	Ala		Val	Ara	Pro	Cvs		Ser	Ile	Glu	Glv		Lvs	Thr	Pro			
	202	_1	130			5		135					140	- 4	4 -					
	203	Tyr	Thr	Asp	Val	Asn	Ile	Val	Thr	Ile	Arg	Glu	Asn	Thr	Glu	Gly	Glu			
	204	145		-			150					155				_	160			
	205	Tyr	Ser	Gly	Ile	Glu	His	Val	Ile	Val	Asp	Gly	Val	Val	${\tt Gln}$	Ser	Ile			
	206					165					170					175		\		
	207	Lys	Leu	Ile		Glu	Glu	Ala	Ser	Lys	Arg	Ile	Ala	Glu		Ala	Ser	,		^
	208				180					185		1	<u>_</u> `	\	190			-	In	4
E>		Ser	Thr		Gly	Thr	Thr	Thr	_	Thr	Thr	Ser		,	Cys	Thr	Lys	$\wedge$	ym	7
	210		_	195		_		_	200		_			205	_	_	_			
	211	Ala		Ile	Met	Arg	Met		Asp	Gly	Leu	Phe		GIn	Lys	Cys	Arg			
	212	<b>a</b> 1	210	<b>a</b>	<b>a1</b>	3	ml	215	T	m 1			220							
	213		ire	Cys	GIY	Arg		val	ьуs	Thr										
	214	225	O TO C	, TD	NO.	0	230													
		<210>																		
		<211><212>				<b>.</b>					- (/	<i>'</i>	)							
		<213>				Mine π	ווופרוי	ilne			U	• /								
		<400>					iusci	1145			•									
	279						ro ac	racco	regat	- aac	atto	ecta	tata	agge	rea a	cago	ctacgc		60	
	280					_	-	-	-		-						gcgag	1	20	
	281																ctttt		.80	
	282																ctgag		240	
	283																gggag		300	
	284																tcagg		60	
	285																tggga	4	20	
						_		_				-	-				_			

RAW SEQUENCE LISTING

DATE: 07/27/2001

PATENT APPLICATION: US/09/559,013A

TIME: 11:32:09

Input Set : A:\473195\_1.txt
Output Set: N:\CRF3\07272001\1559013A.raw

286 gttagggaga ctccggagtg tgattgagtt ggacagccct tctgtgactg ctgagcaggt	480
287 ggctgctatc gagcaagagt gtcaatcaga aaatcagaga eeggctgcct ggtgagtgtt	540
E> 288 cgagagetga netgnatgac cetgaaggtg gaccaggtga agggggnegg ggntttgece	600
E> 289/ gatgaatcaa tgctgggccc attcgagntt nttnccaatc ggaaggtgtt aaaacnccaa	√ 660
E> 290 caatgtgcng tngggaacnc acgtnaagcc aaacctcgnt gaccttcagg tcnattnaaa	720
E> 291 attctggggg anctggaaaa agggnaaaaa agnaccaaaa gccaacctgg atatttcnng	780 1 Xen
E> 2 2 gccgggnanc nggttantga antttggatt ggnnacnnaa ttcctgggaa gttgaaaaag	840
E> 293 cctttgnacc cccctaactt naaantntgn gcattnaaan tn	882
480 <210> SEQ ID NO: 15	
481 <211> LENGTH: 612	
482 <212> TYPE: DNA	
483 <213> ORGANISM: Mus musculus	
485 <400> SEQUENCE: 15	
486 eggeacgage tegtgteete tgegeetgtg teegeegeet geeegeggee ttegegeege	60
E> 487 tgccccggct tcccacnttg gccttggcgc ggccgctcag caccacccta tgccctgagg	120 Jun 9
488 gaatccggag gagacccggg gctctgcagt ccgccttggc gctcgcgcag gtgcctggaa	180
489 cagtcacaca tttgtgccgc cagtacagtg acgcaccccc actgacgtta gaggaatcaa	240
490 ggaccgagtt ctgtatgtct tgaaactcta tgataagatt gatccagaaa agctctccgt	300
491 aaattotoat titatgaagg acctgggott agacagtttg gaccaagtgg aaattattat	360
492 ggccatggaa gacgaatttg ggtttgaaat tcctgatata gatgcagaga agttaatgtg	420
493 tccacaagaa attgtagatt acattgcaga taagaaggat gtgtatgaat aaagtatcag	
494 agccttcttc ctcactgtga ggactccaga ggacacacga tggcatcgtg gccgactgac	480
	480 540
495 ageggetetg tteaacttgt atttaaattg tetgagtgtt ttaccegtta aaaataaate	480 540 600

#### VERIFICATION SUMMARY

PATENT APPLICATION: US/09/559,013A

DATE: 07/27/2001 TIME: 11:32:10

Input Set : A:\473195\_1.txt

Output Set: N:\CRF3\07272001\I559013A.raw

L:159 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5

M:340 Repeated in SeqNo=5

L:209 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6

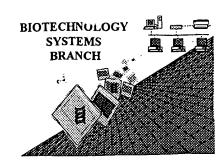
L:288 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9

M:340 Repeated in SeqNo=9

 $L:487\ M:340\ E:$  (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15

Solonan B

# RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/559, 0/3ASource: 1600 Rus HDate Processed by STIC: 9/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker